WHAT IS CLAIMED IS:

1. A recombinant DNA construct comprising a plant centromere.

2. The recombinant DNA construct of claim 1, which additionally comprises a telomere.

3. The recombinant DNA construct of claim 2, wherein the telomere is a plant telomere.

4. The recombinant DNA construct of claim 3, wherein the plant telomere is an *Arabidopsis thaliana* telomere.

5. The recombinant DNA construct of claim 2, wherein the telomere is a yeast telomere.

6. The recombinant DNA construct of claim 1, which additionally comprises an autonomous replicating sequence (ARS).

7. The recombinant DNA construct of claim 6, wherein said ARS is a plant ARS.

8. The recombinant DNA construct of claim 6, wherein said plant ARS is an *Arabidopsis thaliana* ARS.

9. The recombinant DNA construct of claim 1, which additionally comprises a structural gene.

10. The recombinant DNA construct of claim 9, wherein the structural gene comprises a selectable or screenable marker gene.

11. The recombinant DNA construct of claim 9, which additionally comprises a second structural gene.

12. The recombinant DNA construct of claim 9, wherein said structural gene is selected from the group consisting of an antibiotic resistance gene, a herbicide resistance gene, a nitrogen fixation gene, a plant pathogen defense gene, a plant stress-induced gene, a toxin gene, a receptor gene, a ligand gene and a seed storage gene.

13. The recombinant DNA construct of claim 12, wherein said construct is capable of expressing said structural gene.

14. The recombinant DNA construct of claim 13, wherein said construct is capable of expressing said structural gene in a prokaryote.

15. The recombinant DNA construct of claim 13, wherein said construct is capable of expressing said structural gene in a eukaryote.

16. The recombinant DNA construct of claim 15, wherein said eukaryote is a higher eukaryote.

17. The recombinant DNA construct of claim 16, wherein said higher eukaryote is a plant.

18. The recombinant DNA construct of claim 9, wherein said structural gene is selected from the group consisting of a hormone gene, an enzyme gene, an interleukin gene, a clotting factor gene, a cytokine gene, an antibody gene, and a growth factor gene.

19. The recombinant DNA construct of claim 18, wherein said construct is capable of expressing said structural gene.

20. The recombinant DNA construct of claim 19, wherein said construct is capable of expressing said structural gene in a prokaryote.

21. The recombinant DNA construct of claim 19, wherein said construct is capable of expressing said structural gene in a eukaryote.

22. The recombinant DNA construct of claim 21, wherein said eukaryote is a higher eukaryote.

23. The recombinant DNA construct of claim 22, wherein said higher eukaryote is a plant.

24. The recombinant DNA construct of claim 1, further defined as a plasmid.

25. The recombinant DNA construct of claim 24, wherein the plasmid comprises an origin of replication.

26. The recombinant DNA construct of claim 25, wherein the origin of replication functions in bacteria.

27. The recombinant DNA construct of claim 26, wherein the origin of replication functions in *E. coli.*

28. The recombinant DNA construct of claim 26, wherein the origin of replication functions in *Agrobacterium.*

29. The recombinant DNA construct of claim 25, wherein the origin of replication functions in plants.

30. The recombinant DNA construct of claim 25, wherein the origin of replication functions in yeast.

31. The recombinant DNA construct of claim 30, wherein said yeast is *S. cerevisiae*.

32. The recombinant DNA construct of claim 24, wherein the plasmid comprises a selection marker.

33. The recombinant DNA construct of claim 32, wherein the selection marker functions in bacteria.

34. The recombinant DNA construct of claim 32, wherein the selection marker functions in *E. coli*.

35. The recombinant DNA construct of claim 32, wherein the selection marker functions in *Agrobacterium*.

36. The recombinant DNA construct of claim 32, wherein the selection marker functions in plants.

37. The recombinant DNA construct of claim 32, wherein the selection marker functions in yeast.

38. The recombinant DNA construct of claim 37, wherein said yeast is *S. cerevisiae*.

39. The recombinant DNA construct of claim 1, which is capable of being maintained as a chromosome, wherein said chromosome is transmitted in dividing cells.

40. The recombinant DNA construct of claim 1, wherein said plant centromere is an *Arabidopsis thaliana* centromere.

41. The recombinant DNA construct of claim 40, wherein said plant centromere is an *Arabidopsis thaliana* chromosome 1 centromere.

42. The recombinant DNA construct of claim 41, wherein said centromere is flanked by the genetic markers T22C23-T7 and T3P8-SP6.

43. The recombinant DNA construct of claim 42, wherein the centromere is further defined as flanked by the genetic markers T22C23-T7 and T5D18, T22C23-T7 and T3L4, T5D18 and T3P8-SP6, T5D18 and T3L4, and T3L4 and T3P8-SP6.

44. The recombinant DNA construct of claim 40, wherein said plant centromere comprises an *Arabidopsis thaliana* chromosome 2 centromere.

45. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 100 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

46. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 500 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

47. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 1,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

48. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 10,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

49. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 20,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

50. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 40,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

51. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 80,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

52. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 150,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

53. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 300,000 to about 611,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:209.

54. The recombinant DNA construct of claim 44, wherein said centromere comprises the nucleic acid sequence of SEQ ID NO:209.

55. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 100 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

56. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 500 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

57. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 1,000 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

58. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 5,000 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

59. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 10,000 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

60. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 20,000 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

61. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 30,000 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

62. The recombinant DNA construct of claim 44, wherein said centromere comprises from about 40,000 to about 50,959 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:210.

63. The recombinant DNA construct of claim 44, wherein said centromere comprises the nucleic acid sequence of SEQ ID NO:210.

64. The recombinant DNA construct of claim 40, wherein said plant centromere is an *Arabidopsis thaliana* chromosome 3 centromere.

65. The recombinant DNA construct of claim 62, wherein centromere is further defined as flanked by the genetic markers T9G9-SP6 and T5M14-SP6.

66. The recombinant DNA construct of claim 65, wherein the centromere is still further defined as flanked by a pair of genetic markers selected from the group consisting of T9G9-SP6 and TI4H20, T9G9-SP6 and T7K14, T9G9-SP6 and T21P20, T14H20 and T7K14, T14H20 and T21P20, T14H20 and T5M14-SP6, T7K14 and T5M14-SP6, T7K14 and T21P20, and T21P20 and T5M14-SP6.

67. The recombinant DNA construct of claim 40, wherein said plant centromere is an *Arabidopsis thaliana* chromosome 4 centromere.

68. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 100 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

69. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 500 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

70. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 1,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

71. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 5,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

72. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 10,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

73. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 50,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

74. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 100,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

75. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 200,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

76. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 400,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

77. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 800,000 to about 1,082,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:211.

78. The recombinant DNA construct of claim 67, wherein said centromere comprises the nucleic acid sequence of SEQ ID NO:211.

79. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 100 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

80. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 500 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

81. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 1,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

82. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 5,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

83. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 10,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

84. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 30,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

85. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 50,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

86. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 80,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

87. The recombinant DNA construct of claim 67, wherein said centromere comprises from about 120,000 to about 163,317 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:212.

88. The recombinant DNA construct of claim 67, wherein said centromere comprises the nucleic acid sequence of SEQ ID NO:212.

89. The recombinant DNA construct of claim 40, wherein said plant centromere is an *Arabidopsis thaliana* chromosome 5 centromere.

90. The recombinant DNA construct of claim 89, wherein said centromere is flanked by the genetic markers F13K20-T7 and CUE1.

91. The recombinant DNA construct of claim 90, wherein said centromere is flanked by a pair of genetic markers selected from the group consisting of F13K20-T7 and T18M4, F13K20-T7 and T18F2, F13K20-T7 and T24I20, T18M4 and T18F2, T18M4 and T24I20, T18M4 and CUE1, T18F2 and T24I20, T18F2 and CUE1, and T24I20 and CUE1.

92. The recombinant DNA construct of claim 1, comprising n copies of a repeated nucleotide sequence, wherein n is at least 2.

93. The recombinant DNA construct of claim 92, wherein n is from about 5 to about 100,000.

94. The recombinant DNA construct of claim 92, wherein n is from about 10 to about 80,000.

95. The recombinant DNA construct of claim 92, wherein n is from about 25 to about 60,000.

96. The recombinant DNA construct of claim 92, wherein n is from about 100 to about 50,000.

97. The recombinant DNA construct of claim 92, wherein n is from about 200 to about 40,000.

98. The recombinant DNA construct of claim 92, wherein n is from about 400 to about 30,000.

99. The recombinant DNA construct of claim 92, wherein n is from about 1,000 to about 30,000.

100. The recombinant DNA construct of claim 92, wherein n is from about 5,000 to about 20,000.

101. The recombinant DNA construct of claim 92, wherein n is from about 10,000 to about 15,000.

102. The recombinant DNA construct of claim 92, wherein said repeated nucleotide sequence is isolatable from the nucleic acid sequence given by SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211 or SEQ ID NO:212.

103. A minichromosome vector comprising a plant centromere and a telomere sequence.

104. The minichromosome vector of claim 103, comprising an autonomous replicating sequence.

105. The minichromosome vector of claim 103, comprising a second telomere sequence.

106. The minichromosome vector of claim 103, comprising a structural gene.

107. The minichromosome vector of claim 103, further defined as comprising a second structural gene.

108. The minichromosome vector of claim 103, further defined as comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21.

109. A cell transformed with a recombinant DNA construct comprising a plant centromere.

110. The cell of claim 109, wherein said cell is a prokaryotic cell.

111. The cell of claim 109, wherein said cell is a eukaryotic cell.

112. The cell of claim 111, wherein said cell is a yeast cell.

113. The cell of claim 109, wherein said cell is a higher eukaryotic cell.

114. The cell of claim 113, wherein said higher eukaryotic cell is a plant cell.

115. The cell of claim 114, wherein said plant cell is from a dicotyledonous plant.

116. The cell of claim 115, wherein said dicotyledonous plant is selected from the group consisting of group consisting of tobacco, tomato, potato, sugar beet, pea, carrot, cauliflower, broccoli, soybean, canola, sunflower, alfalfa, cotton and *Arabidopsis*.

117. The cell of claim 116, wherein said dicotyledonous plant is *Arabidopsis thaliana*.

118. The cell of claim 114, wherein said plant cell is from a monocotyledonous plant.

119. The cell of claim 118, wherein said monocotyledonous plant is selected from the group consisting of wheat, maize, rye, rice, turfgrass, oat, barley, sorghum, millet, and sugarcane.

120. The cell of claim 109, wherein the plant centromere is an *Arabidopsis thaliana* centromere.

121. The cell of claim 120, further defined as an *Arabidopsis thaliana* cell.

122. The cell of claim 109, wherein said recombinant DNA construct comprises a telomere.

123. The cell of claim 109, wherein said recombinant DNA construct comprises an autonomous replicating sequence (ARS).

124. The cell of claim 109, wherein said recombinant DNA construct comprises a structural gene.

125. The cell of claim 124, wherein the structural gene comprises a selectable or screenable marker gene.

126. The cell of claim 124, wherein said recombinant DNA construct comprises a second structural gene.

127. The cell of claim 124, further defined as capable of expressing said structural gene.

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128. A plant comprising the cell of claim 109.

129. A method of preparing a transgenic plant cell comprising contacting a starting plant cell with a recombinant DNA construct comprising a plant centromere, whereby said starting plant cell is transformed with said recombinant DNA construct.

130. The method of claim 129, wherein said recombinant DNA construct comprises a structural gene.

131. The method of claim 130, wherein the recombinant DNA construct comprises a second structural gene.

132. The method of claim 129, wherein the plant centromere is an *Arabidopsis thaliana* centromere.

133. The method of claim 132, wherein said starting plant cell is an *Arabidopsis thaliana* cell.

134. A transgenic plant comprising a minichromosome vector, wherein said vector comprises a plant centromere and a telomere sequence.

135. The transgenic plant of claim 134, wherein said minichromosome vector comprises an autonomous replicating sequence.

136. The transgenic plant of claim 134, wherein said minichromosome vector comprises a second telomere sequence.

137. The transgenic plant of claim 134, wherein said minichromosome vector comprises a structural gene.

138. The transgenic plant of claim 137, wherein said structural gene is selected from the group consisting of an antibiotic resistance gene, a herbicide resistance gene, a nitrogen fixation gene, a plant pathogen defense gene, a plant stress-induced gene, a toxin gene, a receptor gene, a ligand gene and a seed storage gene.

139. The transgenic plant of claim 137, wherein said first exogenous structural gene is selected from the group consisting of a hormone gene, an enzyme gene, an interleukin gene, a clotting factor gene, a cytokine gene, an antibody gene, and a growth factor gene.

140. The transgenic plant of claim 134, wherein said minichromosome vector comprises a second structural gene.

141. The transgenic plant of claim 134, wherein said minichromosome vector comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21.

142. The transgenic plant of claim 134, further defined as a dicotyledonous plant.

143. The transgenic plant of claim 143, wherein said dicotyledonous plant is selected from the group consisting of tobacco, tomato, potato, sugar beet, pea, carrot, cauliflower, broccoli, soybean, canola, sunflower, alfalfa, cotton and *Arabidopsis*.

144. The transgenic plant of claim 143, wherein the dicotyledonous plant is *Arabidopsis thaliana*.

145. The transgenic plant of claim 134, further defined as a monocotyledonous plant.

146. The transgenic plant of claim 145, wherein said monocotyledonous plant is selected from the group consisting of wheat, maize, rye, rice, turfgrass, oat, barley, sorghum, millet, and sugarcane.

147. A method of producing a minichromosome vector comprising:

(a) obtaining a first vector and a second vector, wherein said first vector or said second vector comprises a selectable or screenable marker, an origin of replication, a telomere, and a plant centromere, and wherein said first vector and said second vector comprises a site for site-specific recombination; and

(b) contacting said first vector with said second vector to allow site-specific recombination to occur between said site for site-specific recombination on said first vector and said site for site-specific recombination on said second vector to create a minichromosome vector comprising said selectable or screenable marker, said origin of replication, said telomere and said plant centromere.

148. The method of claim 147, wherein said contacting is done *in vitro*.

149. The method of claim 148, wherein said contacting is done *in vivo*.

150. The method of claim 149, wherein said contacting is carried out in a prokaryotic cell.

151. The method of claim 150, wherein said prokaryotic cell is an *Agrobacterium* cell.

152. The method of claim 150, wherein said prokaryotic cell is an *E. coli* cell.

153. The method of claim 149, wherein said contacting is carried out in lower eukaryotic cell.

154. The method of claim 153, wherein said lower eukaryotic cell is a yeast cell.

155. The method of claim 149, wherein said contacting is carried out in a higher eukaryotic cell.

156. The method of claim 155, wherein said higher eukaryotic cell is a plant cell.

157. The method of claim 156, wherein said plant cell is an *Arabidopsis thaliana* cell.

158. The method of claim 147, wherein said contacting is done in the presence of a recombinase.

159. The method of claim 158, wherein said recombinase is selected from the group consisting of Cre, Flp, Gin, Pin, Sre, pinD, Int-B13, and R.

160. The method of claim 147, wherein said first vector or said second vector comprises border sequences for *Agrobacterium*-mediated transformation.

161. The method of claim 147, wherein said plant centromere is an *Arabidopsis thaliana* centromere.

162. The method of claim 147, wherein said telomere is a plant telomere.

163. The method of claim 147, wherein said plant selectable or screenable marker is selected from the group consisting of GFP, GUS, BAR, PAT, HPT or NPTII.

164. A method of screening a candidate centromere sequence for plant centromere activity, said method comprising the steps of:

(a) obtaining an isolated nucleic acid sequence comprising a candidate centromere sequence;

(b) integratively transforming plant cells with said isolated nucleic acid; and

(c) screening for centromere activity of said candidate centromere sequence.

165. The method of claim 164, wherein said screening comprises observing a phenotypic effect present in the integratively transformed plant cells or plants comprising said plant cells, wherein said phenotypic effect is absent in a control plant cell not integratively transformed with said isolated nucleic acid sequence, or a plant comprising said control plant cell.

166. The method of claim 165, wherein said phenotypic effect is selected from the group consisting of: reduced viability, reduced efficiency of said transforming, genetic instability in the integratively transformed nucleic acid, aberrant plant sectors, increased ploidy, aneuploidy, and increased integrative transformation in distal or centromeric chromosome regions.

167. The method of claim 164, wherein said isolated nucleic acid sequence comprises a bacterial artificial chromosome.

168. The method of claim 167, wherein said bacterial artificial chromosome is further defined as a binary bacterial artificial chromosome.

169. The method of claim 164, wherein said integratively transforming comprises use of *Agrobacterium*-mediated transformation.

170. The method of claim 164, wherein said control plant cell has been integratively transformed with a nucleic acid sequence other than a candidate centromere sequence.

171. A recombinant DNA construct comprising an *Arabidopsis* polyubiquitin 11 promoter, wherein said promoter comprises from about 25 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

172. The recombinant DNA construct of ~~claim 171~~, wherein said wherein said promoter comprises from about 75 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

173. The recombinant DNA construct of claim 171, wherein said wherein said promoter comprises from about 125 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

174. The recombinant DNA construct of claim 171, wherein said wherein said promoter comprises from about 200 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

175. The recombinant DNA construct of ~~claim 171~~, wherein said wherein said promoter comprises from about 400 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

176. The recombinant DNA construct of claim 171, wherein said wherein said promoter comprises from about 800 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

177. The recombinant DNA construct of claim 171, wherein said wherein said promoter comprises from about 1,000 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:180.

178. The recombinant DNA construct of claim 171, wherein said promoter comprises the nucleic acid sequence of SEQ ID NO:180.

179. The recombinant DNA construct of claim 171, further comprising an enhancer.

180. The recombinant DNA construct of claim 171, further comprising a telomere sequence.

181. The recombinant DNA construct of claim 171, further comprising a plant centromere sequence.

182. The recombinant DNA construct of claim 171, further comprising an ARS.

183. The recombinant DNA construct of claim 171, wherein said promoter is operably linked to a structural gene.

184. The recombinant DNA construct of claim 183, wherein said structural gene is selected from the group consisting of an antibiotic resistance gene, a herbicide resistance gene, a nitrogen fixation gene, a plant pathogen defense gene, a plant stress-induced gene, a toxin gene, a receptor gene, a ligand gene and a seed storage gene.

185. The recombinant DNA construct of claim 183, wherein said structural gene is selected from the group consisting of a hormone gene, an enzyme gene, an interleukin gene, a clotting factor gene, a cytokine gene, an antibody gene, and a growth factor gene.

186. A recombinant DNA construct comprising an *Arabidopsis* 40S ribosomal protein S16 promoter, wherein said promoter comprises from about 25 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

187. The recombinant DNA construct of claim 186, wherein said wherein said promoter comprises from about 75 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

188. The recombinant DNA construct of claim 186, wherein said wherein said promoter comprises from about 125 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

189. The recombinant DNA construct of claim 186, wherein said wherein said promoter comprises from about 200 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

190. The recombinant DNA construct of claim 186, wherein said wherein said promoter comprises from about 400 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

191. The recombinant DNA construct of claim 186, wherein said wherein said promoter comprises from about 800 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

192. The recombinant DNA construct of claim 186, wherein said wherein said promoter comprises from about 1,000 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:182.

193. The recombinant DNA construct of claim 186, wherein said promoter comprises the nucleic acid sequence of SEQ ID NO:182.

194. The recombinant DNA construct of claim 186, further comprising an enhancer.

195. The recombinant DNA construct of claim 186, further comprising a telomere sequence.

196. The recombinant DNA construct of claim 186, further comprising a plant centromere sequence.

197. The recombinant DNA construct of claim 186, further comprising an ARS.

198. The recombinant DNA construct of claim 186, wherein said promoter is operably linked to a structural gene.

199. The recombinant DNA construct of claim 198, wherein said structural gene is selected from the group consisting of an antibiotic resistance gene, a herbicide resistance gene, a nitrogen fixation gene, a plant pathogen defense gene, a plant stress-induced gene, a toxin gene, a receptor gene, a ligand gene and a seed storage gene.

200. The recombinant DNA construct of claim 198, wherein said structural gene is selected from the group consisting of a hormone gene, an enzyme gene, an interleukin gene, a clotting factor gene, a cytokine gene, an antibody gene, and a growth factor gene.

201. A recombinant DNA construct comprising an *Arabidopsis* polyubiquitin 11 3' regulatory sequence, wherein said 3' regulatory sequence comprises from about 25 to about 2001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

202. The recombinant DNA construct of claim 201, wherein said wherein said 3' regulatory sequence comprises from about 75 to about 2001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

203. The recombinant DNA construct of claim 201, wherein said wherein said 3' regulatory sequence comprises from about 125 to about 2001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

204. The recombinant DNA construct of claim 201, wherein said wherein said 3' regulatory sequence comprises from about 200 to about 2001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

205. The recombinant DNA construct of claim 201, wherein said wherein said 3' regulatory sequence comprises from about 400 to about 2001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

206. The recombinant DNA construct of claim 201, wherein said wherein said 3' regulatory sequence comprises from about 800 to about 2001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

207. The recombinant DNA construct of claim 201, wherein said wherein said 3' regulatory sequence comprises from about 1,000 to about 2,001 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:181.

208. The recombinant DNA construct of claim 201, wherein said 3' regulatory sequence comprises the nucleic acid sequence of SEQ ID NO:181.

209. The recombinant DNA construct of claim 201, further comprising an enhancer.

210. The recombinant DNA construct of claim 201, further comprising a telomere sequence.

211. The recombinant DNA construct of claim 201, further comprising a plant centromere sequence.

212. The recombinant DNA construct of claim 201, further comprising an ARS.

213. The recombinant DNA construct of claim 201, wherein said 3' regulatory sequence is operably linked to a structural gene.

214. The recombinant DNA construct of claim 213, wherein said structural gene is selected from the group consisting of an antibiotic resistance gene, a herbicide resistance gene, a nitrogen fixation gene, a plant pathogen defense gene, a plant stress-induced gene, a toxin gene, a receptor gene, a ligand gene and a seed storage gene.

215. The recombinant DNA construct of claim 213, wherein said structural gene is selected from the group consisting of a hormone gene, an enzyme gene, an interleukin gene, a clotting factor gene, a cytokine gene, an antibody gene, and a growth factor gene.

216. A recombinant DNA construct comprising an *Arabidopsis* 40S ribosomal protein S16 3' regulatory sequence, wherein said 3' regulatory comprises from about 25 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

217. The recombinant DNA construct of claim 216, wherein said wherein said 3' regulatory sequence comprises from about 75 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

218. The recombinant DNA construct of claim 216, wherein said wherein said 3' regulatory sequence comprises from about 125 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

219. The recombinant DNA construct of claim 216, wherein said wherein said 3' regulatory sequence comprises from about 200 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

220. The recombinant DNA construct of claim 216, wherein said wherein said 3' regulatory sequence comprises from about 400 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

221. The recombinant DNA construct of claim 216, wherein said wherein said 3' regulatory sequence comprises from about 800 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

222. The recombinant DNA construct of claim 216, wherein said wherein said 3' regulatory sequence comprises from about 1,000 to about 2,000 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:183.

223. The recombinant DNA construct of claim 216, wherein said 3' regulatory sequence comprises the nucleic acid sequence of SEQ ID NO:183.

224. The recombinant DNA construct of claim 216, further comprising an enhancer.

225. The recombinant DNA construct of claim 216, further comprising a telomere sequence.

226. The recombinant DNA construct of claim 216, further comprising a plant centromere sequence.

227. The recombinant DNA construct of claim 216, further comprising an ARS.

228. The recombinant DNA construct of claim 216, wherein said 3' regulatory sequence is operably linked to a structural gene.

229. The recombinant DNA construct of claim 228, wherein said structural gene is selected from the group consisting of an antibiotic resistance gene, a herbicide resistance gene, a nitrogen fixation gene, a plant pathogen defense gene, a plant stress-induced gene, a toxin gene, a receptor gene, a ligand gene and a seed storage gene.

230. The recombinant DNA construct of claim 228, wherein said structural gene is selected from the group consisting of a hormone gene, an enzyme gene, an interleukin gene, a clotting factor gene, a cytokine gene, an antibody gene, and a growth factor gene.

231. The recombinant DNA construct of claim 67, wherein said centromere comprises at least about 100 contiguous nucleotides of the nucleic acid sequence selected from the group consisting of SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, and SEQ ID NO:208.